

Thurs., 4/15/04

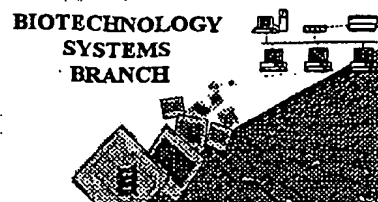
TO: Ms. Francine Young, PCT

FROM: Anne-Marie Corrigan, STIC

Ms. Young:

Per your request, enclosed is the error report for 09/856,451. Thank you.

Total: 9 pages includes cover sheet



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/856,451
Source: 29/09
Date Processed by STIC: 4/14/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA. 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTEDSUGGESTED CORRECTIONSERIAL NUMBER: 09/856,451

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC - Biotechnology Systems Branch - 09/09/2003



PCT09

RAW SEQUENCE LISTING

DATE: 04/14/2004

PATENT APPLICATION: US/09/856,451

TIME: 10:35:47

Input Set : A:\X-12553 Sequence Listing.txt

Output Set: N:\CRF4\04142004\I856451.raw

3 <110> APPLICANT: Eli Lilly and Company
4 Beals, John
6 <120> TITLE OF INVENTION: ERYTHROPOIETIC COMPOUNDS
8 <130> FILE REFERENCE: X-12553
10 <140> CURRENT APPLICATION NUMBER: US 09/856,451
C--> 11 <141> CURRENT FILING DATE: 2003-01-09
13 <150> PRIOR APPLICATION NUMBER: PCT/US99/27801
14 <151> PRIOR FILING DATE: 1999-11-23
16 <160> NUMBER OF SEQ ID NOS: 4
18 <170> SOFTWARE: PatentIn version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 168
22 <212> TYPE: PRT
23 <213> ORGANISM: synthetic construct
25 <220> FEATURE:
26 <221> NAME/KEY: VARIANT
27 <222> LOCATION: (1)..(1)
28 <223> OTHER INFORMATION: Xaa at position 1 is absent or Met;
31 <220> FEATURE:
32 <221> NAME/KEY: VARIANT
33 <222> LOCATION: (2)..(2)
34 <223> OTHER INFORMATION: Xaa at position 2 is absent or is Ala, Cys, Asp, Glu, Phe,
Gly, H
35 is Ile, Leu, Met, Asn, Gln, Arg, Ser, Thr, Val, Trp, or Tyr
38 <220> FEATURE:
39 <221> NAME/KEY: VARIANT
40 <222> LOCATION: (26)..(26)
41 <223> OTHER INFORMATION: Xaa at position 26 is Asn, Lys or Glu;
44 <220> FEATURE:
45 <221> NAME/KEY: VARIANT
46 <222> LOCATION: (40)..(40)
47 <223> OTHER INFORMATION: Xaa at position 40 is Asn, Lys or Glu;
50 <220> FEATURE:
51 <221> NAME/KEY: VARIANT
52 <222> LOCATION: (78)..(78)
53 <223> OTHER INFORMATION: Xaa at position 78 is Arg or Glu;
56 <220> FEATURE:
57 <221> NAME/KEY: VARIANT
58 <222> LOCATION: (85)..(85)
59 <223> OTHER INFORMATION: Xaa at position 85 is Asn, Lys or Glu;
62 <220> FEATURE:
63 <221> NAME/KEY: VARIANT
64 <222> LOCATION: (90)..(90)
65 <223> OTHER INFORMATION: Xaa at position 90 is Trp, Lys, Pro, or Arg;

pp 1, 3-4
Does Not Comply
Corrected Diskette Needed

invalid <213> response - see item 10
on Error Summary
Sheet.

RAW SEQUENCE LISTING

DATE: 04/14/2004

PATENT APPLICATION: US/09/856,451

TIME: 10:35:47

Input Set : A:\X-12553 Sequence Listing.txt

Output Set: N:\CRF4\04142004\I856451.raw

68 <220> FEATURE:
69 <221> NAME/KEY: VARIANT
70 <222> LOCATION: (128)..(128)
71 <223> OTHER INFORMATION: Xaa at position 128 is Ser, Thr, Lys or Glu;
74 <220> FEATURE:
75 <221> NAME/KEY: VARIANT
76 <222> LOCATION: (141)..(141)
77 <223> OTHER INFORMATION: Xaa at position 141 is Arg or Glu;
80 <220> FEATURE:
81 <221> NAME/KEY: VARIANT
82 <222> LOCATION: (156)..(156)
83 <223> OTHER INFORMATION: Xaa at position 156 is Lys or Glu; and
86 <220> FEATURE:
87 <221> NAME/KEY: VARIANT
88 <222> LOCATION: (168)..(168)
89 <223> OTHER INFORMATION: Xaa at position 168 is Arg, absent, or any other amino acid.
92 <400> SEQUENCE: 1
W--> 94 Xaa Xaa Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg
95 1 5 10 15
97 Tyr Leu Leu Glu Ala Lys Glu Ala Glu Xaa Ile Thr Thr Gly Cys Ala
98 20 25 30
100 Glu His Cys Ser Leu Asn Glu Xaa Ile Thr Val Pro Asp Thr Lys Val
101 35 40 45
103 Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu
104 50 55 60
106 Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Xaa Gly Gln
107 65 70 75 80
109 Ala Leu Leu Val Xaa Ser Ser Gln Pro Xaa Glu Pro Leu Gln Leu His
110 85 90 95
112 Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg
113 100 105 110
115 Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Xaa
116 115 120 125
118 Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Xaa Lys Leu Phe
119 130 135 140
121 Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Xaa Leu Tyr Thr Gly
122 145 150 155 160
124 Glu Ala Cys Arg Thr Gly Asp Xaa
125 165
127 <210> SEQ ID NO: 2
128 <211> LENGTH: 193
129 <212> TYPE: PRT
130 <213> ORGANISM: Homo sapiens
132 <400> SEQUENCE: 2
134 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
135 1 5 10 15
137 Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
138 20 25 30
140 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu

RAW SEQUENCE LISTING

DATE: 04/14/2004

PATENT APPLICATION: US/09/856,451

TIME: 10:35:47

Input Set : A:\X-12553 Sequence Listing.txt

Output Set: N:\CRF4\04142004\I856451.raw

141 35 40 45
143 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
144 50 55 60
146 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
147 65 70 75 80
149 Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
150 85 90 95
152 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
153 100 105 110
155 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
156 115 120 125
158 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
159 130 135 140
161 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
162 145 150 155 160
164 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
165 165 170 175
167 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
168 180 185 190
170 Arg
173 <210> SEQ ID NO: 3
174 <211> LENGTH: 498
175 <212> TYPE: DNA
176 <213> ORGANISM: synthetic construct
178 <220> FEATURE:
179 <221> NAME/KEY: CDS
180 <222> LOCATION: (1)..(495)
182 <400> SEQUENCE: 3
183 gct cca cca cgt ctt att tgt gat tct cgt gtt ctt gaa cgt tac ctg 48
184 Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
185 1 5 10 15
187 ctg gaa gct aaa gaa gct gaa aac atc acc acc ggt tgc gct gaa cac 96
188 Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
189 20 25 30
191 tgc tcc ctg aac gaa aac atc acc gtt ccg gac acc aaa gtt aac ttc 144
192 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
193 35 40 45
195 tac gct tgg aaa cgt atg gaa gtt ggt cag cag gct gtt gaa gtt tgg 192
196 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
197 50 55 60
199 cag ggt ctg gct ctg ctg tcc gaa gct gtt ctg cgt ggt cag gct ctg 240
200 Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
201 65 70 75 80
203 ctg gtt aac tcc tcc cag ccg tgg gaa ccg ctg cag ctg cac gtt gac 288
204 Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
205 85 90 95
207 aaa gct gtt tcc ggt ctg cgt tcc ctg acc acc ctg ctg cgt gct ctg 336
208 Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
209 100 105 110

invalid response

RAW SEQUENCE LISTING

DATE: 04/14/2004

PATENT APPLICATION: US/09/856,451

TIME: 10:35:47

Input Set : A:\X-12553 Sequence Listing.txt

Output Set: N:\CRF4\04142004\I856451.raw

211 ggt gct cag aaa gaa gct atc tcc ccg ccg gac gct gct tcc gct gct 384
212 Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
213 115 120 125
215 ccg ctg cgt acc atc acc gct gac acc ttc cgt aaa ctg ttc cgt gtt 432
216 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
217 130 135 140
219 tac tcc aac ttc ctg cgt ggt aaa ctg aaa ctg tac acc ggt gaa gct 480
220 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
221 145 150 155 160
223 tgc cgt acc ggt gac tga 498
224 Cys Arg Thr Gly Asp
225 165
228 <210> SEQ ID NO: 4
229 <211> LENGTH: 165
230 <212> TYPE: PRT
231 <213> ORGANISM: synthetic construct *invalid*
233 <400> SEQUENCE: 4
235 Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
236 1 5 10 15
239 Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
240 20 25 30
243 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
244 35 40 45
247 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
248 50 55 60
251 Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
252 65 70 75 80
255 Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
256 85 90 95
259 Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
260 100 105 110
263 Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
264 115 120 125
267 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
268 130 135 140
271 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
272 145 150 155 160
275 Cys Arg Thr Gly Asp
276 165

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/856,451

DATE: 04/14/2004
TIME: 10:35:48

Input Set : A:\X-12553 Sequence Listing.txt
Output Set: N:\CRF4\04142004\I856451.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1, 2, 28, 40, 76, 85, 90, 128, 141, 156, 168

VERIFICATION SUMMARY

DATE: 04/14/2004

PATENT APPLICATION: US/09/856,451

TIME: 10:35:48

Input Set : A:\X-12553 Sequence Listing.txt

Output Set: N:\CRF4\04142004\I856451.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0

M:341 Repeated in SeqNo=1

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